

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 5, 2004, 11:38:24 ; Search time 22.225 Seconds  
(without alignments)  
1114.895 Million cell updates/sec

Title: US-09-840-795-17

Perfect score: 77  
Sequence: 1 MDCGENEYMDWGRCTVTCOR.....CQCITCAVINRQKVLHS 77

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1351062 seqs, 321799191 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	73	94.8	173	12	US-10-660-968-38
3	73	94.8	197	10	US-09-796-753-10
4	73	94.8	206	10	US-09-796-753-8
5	73	94.8	231	9	US-09-840-795-19
6	73	94.8	267	12	US-10-660-968-29
7	73	94.8	268	12	US-10-231-416-1
8	73	94.8	268	14	US-10-231-416-1
9	73	94.8	269	12	US-10-660-968-2
10	73	94.8	297	12	US-10-660-968-27
11	73	94.8	299	12	US-10-660-968-35
12	56	72.7	297	14	US-10-243-157-6
13	56	72.7	299	13	US-10-119-466-12
14	56	72.7	299	14	US-10-243-157-3
15	56	72.7	299	14	US-10-413-053-12

16	47	61.0	132	9	US-09-840-795-15	Sequence 15, Appl
17	40	51.9	231	14	US-10-046-433-61	Sequence 61, Appl
18	11	14.3	159	14	US-10-046-433-7	Sequence 7, Appl
19	11	14.3	226	14	US-10-046-433-5	Sequence 5, Appl
20	7	9.1	327	12	US-10-282-122A-46737	Sequence 46737, A
21	7	9.1	362	12	US-10-282-122A-60626	Sequence 60626, A
22	7	9.1	366	12	US-10-282-122A-45735	Sequence 45735, A
23	6	7.8	312	12	US-10-437-963-152312	Sequence 152312, A
24	6	7.8	46	16	US-10-437-963-152312	Sequence 152312, A
25	6	7.8	60	16	US-10-437-963-152312	Sequence 152312, A
26	6	7.8	68	16	US-10-437-963-152312	Sequence 152312, A
27	6	7.8	68	14	US-10-040-862-721	Sequence 721, App
28	6	7.8	68	15	US-10-057-4758-721	Sequence 721, App
29	6	7.8	68	15	US-10-154-8848-721	Sequence 721, App
30	6	7.8	68	16	US-10-764-324-721	Sequence 721, App
31	6	7.8	69	9	US-09-864-761-37930	Sequence 37930, A
32	6	7.8	69	12	US-10-425-114-38115	Sequence 38115, A
33	6	7.8	73	10	US-10-424-599-185073	Sequence 185073, A
34	6	7.8	73	10	US-09-820-843A-82	Sequence 82, Appl
35	6	7.8	75	12	US-10-424-599-155355	Sequence 155355, A
36	6	7.8	75	16	US-10-437-963-111013	Sequence 111013, A
37	6	7.8	76	12	US-10-424-599-243706	Sequence 243706, A
38	6	7.8	76	16	US-10-437-963-117297	Sequence 117297, A
39	6	7.8	77	16	US-10-437-963-117104	Sequence 117104, A
40	6	7.8	87	16	US-10-437-963-203420	Sequence 203420, A
41	6	7.8	89	12	US-10-424-599-227607	Sequence 227607, A
42	6	7.8	97	16	US-10-437-963-128054	Sequence 128054, A
43	6	7.8	109	12	US-10-425-114-36881	Sequence 36881, A
44	6	7.8	114	16	US-10-437-963-112948	Sequence 112948, A
45	6	7.8	126	12	US-10-424-599-171961	Sequence 171961, A

#### ALIGNMENTS

RESULT 1  
US-09-840-795-17  
Sequence 17, Application US/09840795  
Patent No. US20020143147A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Erin B.  
APPLICANT: Mattson, Jeanine D.  
APPLICANT: Bates, Elizabeth Esther Mary  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Ledecque, Serge J.E.  
TITLE OF INVENTION: Mammalian Genes; Related Reagents  
FILE REFERENCE: SF0818X  
CURRENT APPLICATION NUMBER: US/09/840,795  
CURRENT FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: 09/351,777  
PRIOR FILING DATE: 1999-07-12  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 77  
TYPE: PRT  
ORGANISM: Primate  
US-09-840-795-17

Query Match 100.0%; Score 77; DB 9; Length 77;  
Best Local Similarity 100.0%; Pred. No. 3.1e-72;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDCGENEYMDWGRCTVTCORCGPQBLSKDCGVEGDAYCTACPPRRYSKSWGHHKCS 60  
QY CITCAVINRQKVLHS 77  
DB CITCAVINRQKVLHS 77  
61 CITCAVINRQKVLHS 77

RESULT 2

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 5, 2004, 09:43:43 ; Search time 12.95 Seconds  
(without alignments)  
306.965 Million cell updates/sec

Title: US-09-840-795-17

Perfect score: 464

Sequence: 1 MDC09NEMWDMGRCVTCOR.....CSCITCAVINRQVKVLS 77

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:\*

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4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/6C\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	440	94.8	299	4	US-09-548-130-3
3	440	94.8	299	4	US-10-119-466-12
4	245	52.8	210	3	US-09-286-529-3
5	234.5	50.5	151	3	US-09-286-529-4
6	126.5	27.3	448	4	US-09-342-681C-17
7	126.5	27.3	448	4	US-09-342-681C-19
8	106	22.8	415	3	US-09-006-353A-6
9	106	22.8	415	3	US-09-573-986-6
10	102	22.0	169	3	US-08-630-172-11
11	102	22.0	169	3	US-09-375-418-11
12	101.5	21.9	625	3	US-08-996-139-15
13	101.5	21.9	625	3	US-08-995-659-15
14	101.5	21.9	625	3	US-09-215-649A-15
15	101.5	21.9	625	4	US-09-577-780-15
16	101.5	21.9	625	4	US-09-577-800-15
17	101.5	21.9	625	4	US-09-466-496-15
18	101.5	21.9	625	4	US-09-871-856-15
19	101.5	21.9	625	4	US-09-871-291-15
20	101.5	21.9	625	4	US-09-877-650-15
21	98.5	21.2	121	4	US-08-828-683A-18
22	98.5	21.2	260	3	US-09-006-353A-8
23	98.5	21.2	260	3	US-09-573-986-8
24	98.5	21.2	451	3	US-08-996-139-4
25	98.5	21.2	451	3	US-08-995-659-4
26	98.5	21.2	451	3	US-09-215-649A-4
27	98.5	21.2	451	4	US-09-577-780-4

28	98.5	21.2	451	4	US-09-577-800-4	Sequence 4, Appli
29	98.5	21.2	451	4	US-09-466-496-4	Sequence 4, Appli
30	98.5	21.2	451	4	US-09-871-856-4	Sequence 4, Appli
31	98.5	21.2	451	4	US-09-871-291-4	Sequence 4, Appli
32	98.5	21.2	451	4	US-09-877-650-4	Sequence 4, Appli
33	98.5	21.2	451	3	US-08-996-139-2	Sequence 2, Appli
34	98.5	21.2	451	3	US-08-995-659-2	Sequence 2, Appli
35	98.5	21.2	451	3	US-09-215-649A-2	Sequence 2, Appli
36	98.5	21.2	591	4	US-09-577-780-2	Sequence 2, Appli
37	98.5	21.2	591	4	US-09-577-800-2	Sequence 2, Appli
38	98.5	21.2	591	4	US-09-466-496-2	Sequence 2, Appli
39	98.5	21.2	591	4	US-09-871-856-2	Sequence 2, Appli
40	98.5	21.2	591	4	US-09-871-291-2	Sequence 2, Appli
41	98.5	21.2	616	3	US-09-877-650-2	Sequence 2, Appli
42	98.5	21.2	616	3	US-08-996-139-6	Sequence 6, Appli
43	98.5	21.2	616	3	US-08-995-659-6	Sequence 6, Appli
44	98.5	21.2	616	3	US-09-215-649A-6	Sequence 6, Appli
45	98.5	21.2	616	4	US-09-577-780-6	Sequence 6, Appli

## ALIGNMENTS

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RESULT 1
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; FILE REFERENCE: P1739R1
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Human
US-09-548-130-6

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Best Local Similarity 98.6%; Pred. No. 1.3e-40;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      61 CITCAVINRQVKV 73
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DB      61 CITCAVINRQVKV 73
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RESULT 2
US-09-548-130-3
; Sequence 3, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; FILE REFERENCE: P1739R1
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
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OM protein - protein search, using sw model

Run on: October 5, 2004, 11:05:18 ; Search time 30.975 Seconds  
(without alignments)  
799.953 Million cell updates/sec

Title: US-09-840-795-17

Perfect score: 464  
Sequence: 1 MDCQENRYMDQRCVTCOR.....CQCSCITAVINRYQVKQLHS 77

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	100.0	77	9	US-09-840-795-17
2	443	95.5	173	12	US-10-660-968-38
3	443	95.5	197	10	US-09-796-753-10
4	443	95.5	206	10	US-09-796-753-8
5	443	95.5	231	9	US-09-840-795-19
6	443	95.5	267	12	US-10-660-968-29
7	443	95.5	268	14	US-10-231-416-1
8	443	95.5	268	14	US-10-231-416-1
9	443	95.5	269	12	US-10-660-968-2
10	443	95.5	297	12	US-10-660-968-27
11	443	95.5	299	12	US-10-660-968-35
12	440	94.8	297	14	US-10-243-157-6
13	440	94.8	299	13	US-10-119-466-12
14	440	94.8	299	14	US-10-243-157-3
15	440	94.8	299	14	US-10-413-053-12

16	394	84.9	231	14	US-10-046-433-61	Sequence 61, App1
17	298	64.2	132	9	US-09-840-795-15	Sequence 17, App1
18	245	52.8	150	9	US-09-782-980-27	Sequence 27, App1
19	245	52.8	150	9	US-09-840-795-13	Sequence 13, App1
20	245	52.8	150	5	US-10-303-502-1	Sequence 1, App1
21	245	52.8	150	16	US-10-806-018-27	Sequence 27, App1
22	245	52.8	210	9	US-09-877-156-3	Sequence 3, App1
23	245	52.8	214	9	US-09-782-980-23	Sequence 23, App1
24	245	52.8	214	15	US-10-303-502-2	Sequence 2, App1
25	245	52.8	214	16	US-10-806-018-23	Sequence 23, App1
26	245	52.8	416	9	US-09-780-532-6	Sequence 6, App1
27	244	52.6	150	5	US-10-303-502-9	Sequence 9, App1
28	244	52.6	417	9	US-09-780-532-2	Sequence 2, App1
29	244	52.6	417	12	US-10-206-915-474	Sequence 474, App
30	244	52.6	417	12	US-10-199-670-474	Sequence 474, App
31	244	52.6	417	12	US-10-201-858-474	Sequence 474, App
32	244	52.6	417	12	US-10-081-056-290	Sequence 290, App
33	244	52.6	417	12	US-10-219-535-220	Sequence 220, App
34	244	52.6	417	12	US-10-232-230-220	Sequence 220, App
35	244	52.6	417	12	US-10-205-890-474	Sequence 474, App
36	244	52.6	417	12	US-10-208-024-474	Sequence 474, App
37	244	52.6	417	12	US-10-201-853-474	Sequence 474, App
38	244	52.6	417	12	US-10-174-581-474	Sequence 474, App
39	244	52.6	417	12	US-10-176-483-474	Sequence 474, App
40	244	52.6	417	12	US-10-176-749-474	Sequence 474, App
41	244	52.6	417	12	US-10-176-914-474	Sequence 474, App
42	244	52.6	417	12	US-10-176-915-474	Sequence 474, App
43	244	52.6	417	12	US-10-176-484-474	Sequence 474, App
44	244	52.6	417	12	US-10-180-550-474	Sequence 474, App
45	244	52.6	417	12	US-10-183-014-474	Sequence 474, App

#### ALIGNMENTS

RESULT 1  
US-09-840-795-17  
Sequence 17, Application US/09840795  
Patent No. US20020143147A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Erin E.  
APPLICANT: Matteson, Jeanine D.  
APPLICANT: Bates, Elizabeth Bethel Mary  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Lebecque, Serge J.E.  
TITLE OF INVENTION: Mammalian Genes; Related Reagents  
FILE REFERENCE: SF0818X  
CURRENT APPLICATION NUMBER: US/09/840,795  
CURRENT FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: 09/351,777  
PRIOR FILING DATE: 1999-07-12  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 17  
LENGTH: 77  
TYPE: PRT  
ORGANISM: primate  
US-09-840-795-17

Query Match 100.0%; Score 464; DB 9; Length 77;  
Best Local Similarity 100.0%; Pred. No. 26-41;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCQENRYMDQRCVTCORCGPQELSKDCGEGGADYCTACPPRRYSNGHHKCS 60  
DB 1 MDCQENRYMDQRCVTCORCGPQELSKDCGEGGADYCTACPPRRYSNGHHKCS 60

QY 61 CITCAVINRYQVKQLHS 77  
DB 61 CITCAVINRYQVKQLHS 77

RESULT 2

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2004, 11:24:28 / Search time 8.05 Seconds  
(without alignments)  
493.814 Million cell updates/sec

Title: US-09-840-795-17

Perfect score: 77  
Sequence: 1 MDCGENTYDQWGRCTVCR.....CQCITCAVIRVQKVLHS 77

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	72.7	297	4 US-09-548-130-6	Sequence 6, Appl1
2	56	72.7	299	4 US-09-548-130-3	Sequence 3, Appl1
3	56	72.7	299	4 US-10-119-466-12	Sequence 12, Appl1
4	6	7.8	223	4 US-09-252-991A-20528	Sequence 20528, A
5	6	7.8	266	4 US-09-543-681A-5038	Sequence 5038, Ap
6	6	7.8	275	4 US-09-252-991A-18717	Sequence 18717, A
7	6	7.8	337	4 US-09-252-991A-28595	Sequence 28595, A
8	6	7.8	346	2 US-08-744-779A-2	Sequence 2, Appl1
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10	6	7.8	356	4 US-09-252-991A-25656	Sequence 25656, A
11	6	7.8	388	4 US-09-540-226-3444	Sequence 3444, Ap
12	6	7.8	393	4 US-09-194-905-13	Sequence 13, Appl1
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14	6	7.8	420	4 US-09-252-991A-29544	Sequence 29544, A
15	6	7.8	426	4 US-09-972-784-2	Sequence 2, Appl1
16	6	7.8	440	4 US-09-252-991A-19593	Sequence 19593, A
17	6	7.8	443	4 US-09-543-681A-5452	Sequence 5452, Ap
18	6	7.8	460	4 US-09-252-991A-27768	Sequence 27768, A
19	6	7.8	566	4 US-09-489-039A-8217	Sequence 8217, Ap
20	6	7.8	604	4 US-09-489-039A-8519	Sequence 8519, Ap
21	6	7.8	643	4 US-09-252-991A-22490	Sequence 22490, A
22	6	7.8	686	4 US-09-489-039A-13507	Sequence 13507, A
23	6	7.8	742	4 US-09-252-991A-29239	Sequence 29239, A
24	6	7.8	746	4 US-09-548-797B-4	Sequence 4, Appl1
25	6	7.8	787	2 US-08-720-484A-4	Sequence 4, Appl1
26	6	7.8	787	3 US-08-953-823A-4	Sequence 4, Appl1
27	6	7.8	787	4 US-09-398-239-4	Sequence 4, Appl1

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34	6	7.8	793	4 US-09-293-505-16	Sequence 2, Appl1
35	6	7.8	793	4 US-09-560-876A-2	Sequence 2, Appl1
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38	6	7.8	812	4 US-09-632-098-4	Sequence 4, Appl1
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41	6	7.8	915	4 US-09-543-681A-5334	Sequence 5334, Ap
42	6	7.8	978	2 US-08-415-593-43	Sequence 43, Appl1
43	6	7.8	1049	4 US-09-252-991A-17298	Sequence 17298, A
44	6	7.8	3256	4 US-09-919-172-98	Sequence 98, Appl1
45	6	7.8	3256	4 US-09-976-594-22	Sequence 22, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-548-130-6
: Sequence 6, Application US/09548130
: Patent No. 6534061
: GENERAL INFORMATION:
: APPLICANT: Goddard, Audrey
: APPLICANT: Pan, James
: TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
: FILE REFERENCE: P17391
: CURRENT APPLICATION NUMBER: US/09/548,130
: EARLIER FILING DATE: 2000-04-12
: EARLIER APPLICATION NUMBER: US 60/128,849
: EARLIER FILING DATE: 1999-04-12
: NUMBER OF SEQ ID NOS: 13
: SEQ ID NO 6
: LENGTH: 297
: TYPE: PRT
: ORGANISM: Human
US-09-548-130-6

Query Match      72.7%; Score 56; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MDCGENTYDQWGRCTVCRGPGQELSKDGGEGDAYCTACPPRRYSSWGH 56

RESULT 2
US-09-548-130-3
: Sequence 3, Application US/09548130
: Patent No. 6534061
: GENERAL INFORMATION:
: APPLICANT: Goddard, Audrey
: APPLICANT: Pan, James
: APPLICANT: Yan, Minhong
: TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
: FILE REFERENCE: P17391
: CURRENT APPLICATION NUMBER: US/09/548,130
: EARLIER FILING DATE: 2000-04-12
: EARLIER APPLICATION NUMBER: US 60/128,849
: EARLIER FILING DATE: 1999-04-12
: NUMBER OF SEQ ID NOS: 13
: SEQ ID NO 3
: LENGTH: 299
: TYPE: PRT

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